

## SEQUENCE LISTING

DT09 Rec'd PCT/PTO 09 SEP 2004

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 Medical and Biological Laboratories Co., Ltd.  
 Japan Science and Technology Agency  
 Ginkgo Biomedical Research Institute Co., Ltd.

<120> Cdc7-ASK Kinase Complex, Substrates of the Kinase Complex,  
 Specific Antibodies to the Substrates, and Screening Methods  
 Using the Same to Screen for Compounds Comprising Cdc7-ASK  
 Kinase Inhibitory Ability

<130> 082368-001100US

<140> US Not yet assigned  
 <141> Not yet assigned

<150> JP 2002-067702  
 <151> 2002-03-12

<150> WO PCT/JP03/02918  
 <151> 2003-03-12

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<170> PatentIn Ver. 2.1

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Leu	Asp	Asp	Glu	Asp	Val	Glu	Glu	Leu	Thr	Ala	Ser	Gln	Arg	Glu	Ala	
			100					105					110			
gct	gag	cgg	acc	atg	agg	cag	cgg	gac	cgt	gag	gct	ggc	aga	ggc	ctg	384
Ala	Glu	Arg	Thr	Met	Arg	Gln	Arg	Asp	Arg	Glu	Ala	Gly	Arg	Gly	Leu	
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gga	cgc	atg	cgc	cgg	ggg	ctg	ctc	tat	gac	agc	agc	gag	gaa	gat	gag	432
Gly	Arg	Met	Arg	Arg	Gly	Leu	Leu	Tyr	Asp	Ser	Ser	Glu	Glu	Asp	Glu	
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Glu	Arg	Pro	Ala	Arg	Lys	Arg	Arg	His	Val	Glu	Arg	Ala	Thr	Glu	Asp	
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ggc	gag	gag	gat	gaa	gag	atg	atc	gag	agt	att	gag	aat	ctg	gag	gac	528
Gly	Glu	Glu	Asp	Glu	Glu	Met	Ile	Glu	Ser	Ile	Glu	Asn	Leu	Glu	Asp	
				165				170						175		



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Leu Lys Gly His Ser Val Arg Glu Arg Val Ser Met Ala Gly Pro Arg	
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ctg gag atc cac cac cgc ttc aag aac ttc ctg cgc acc cac gtg gac	624
Leu Glu Ile His His Arg Phe Lys Asn Phe Leu Arg Thr His Val Asp	
195 200 205	
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Ser His Gly His Asn Val Phe Lys Glu Arg Ile Ser Asp Met Cys Lys	
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Glu Asn Arg Glu Ser Leu Val Val Asn Tyr Glu Asp Leu Ala Ala Arg	
225 230 235 240	
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Glu His Val Leu Ala Tyr Phe Leu Pro Glu Ala Pro Ala Glu Leu Leu	
245 250 255	
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Gln Ile Phe Asp Glu Ala Ala Leu Glu Val Val Leu Ala Met Tyr Pro	
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aaa tat gac cgt atc acc aac cac atc cat gtg cgc atc tcc cac ctg	864
Lys Tyr Asp Arg Ile Thr Asn His Ile His Val Arg Ile Ser His Leu	
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Pro Leu Val Glu Glu Leu Arg Ser Leu Arg Gln Leu His Leu Asn Gln	
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Leu Ile Arg Thr Ser Gly Val Val Thr Ser Cys Thr Gly Val Leu Pro	
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Gln Leu Ser Met Val Lys Tyr Asn Cys Ser Lys Cys Asn Phe Val Leu	
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Gly Pro Phe Cys Gln Ser Gln Asn Gln Glu Val Lys Pro Gly Ser Cys	
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cct gag tgc cag tct gct ggg ccc ttt gag atc aac atg gag gag acc	1104
Pro Glu Cys Gln Ser Ala Gly Pro Phe Glu Ile Asn Met Glu Glu Thr	
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atc tat cag aac tac caa cgt atc cgc atc cag gag agt ccc ggc aag	1152
Ile Tyr Gln Asn Tyr Gln Arg Ile Arg Ile Gln Glu Ser Pro Gly Lys	
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Val Ala Ala Gly Arg Leu Pro Arg Ser Lys Asp Ala Ile Leu Leu Ala	
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Asp Leu Val Asp Ser Cys Lys Pro Gly Asp Glu Ile Glu Leu Thr Gly	
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Ile Tyr His Asn Asn Tyr Asp Gly Ser Leu Asn Thr Ala Asn Gly Phe	
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Pro Val Phe Ala Thr Ile Ile Leu Ala Asn His Val Ala Lys Lys Asp	
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Asn Lys Val Ala Val Gly Glu Leu Thr Asp Glu Asp Val Lys Met Ile	
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Thr Gly Leu Ser Lys Asp Gln Gln Ile Gly Glu Lys Ile Phe Ala Ser	
465 470 475 480	
att gca ccc tcc atc tat ggg cat gaa gac atc aag aga ggc ctg gct	1488
Ile Ala Pro Ser Ile Tyr Gly His Glu Asp Ile Lys Arg Gly Leu Ala	
485 490 495	
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Leu Ala Leu Phe Gly Gly Glu Pro Lys Asn Pro Gly Gly Lys His Lys	
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Val Arg Gly Asp Ile Asn Val Leu Leu Cys Gly Asp Pro Gly Thr Ala	
515 520 525	
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Lys Ser Gln Phe Leu Lys Tyr Ile Glu Lys Val Ser Ser Arg Ala Ile	
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Phe Thr Thr Gly Gln Gly Ala Ser Ala Val Gly Leu Thr Ala Tyr Val	
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Gln Arg His Pro Val Ser Arg Glu Trp Thr Leu Glu Ala Gly Ala Leu	
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Val Leu Ala Asp Arg Gly Val Cys Leu Ile Asp Glu Phe Asp Lys Met	
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Asn Asp Gln Asp Arg Thr Ser Ile His Glu Ala Met Glu Gln Gln Ser	
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Ile Ser Ile Ser Lys Ala Gly Ile Val Thr Ser Leu Gln Ala Arg Cys	
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Thr Val Ile Ala Ala Ala Asn Pro Ile Gly Gly Arg Tyr Asp Pro Ser	
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ctg acc ttc tca gag aat gta gac ctc aca gag ccc atc att tcc cgc	1968
Leu Thr Phe Ser Glu Asn Val Asp Leu Thr Glu Pro Ile Ile Ser Arg	
645 650 655	

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Phe Asp Val Leu Cys Val Val Arg Asp Thr Val Asp Pro Val Gln Asp	
660 665 670	
gag atg ctg gcc cgc ttt gtg gtt ggc agc cac gtc aga cac cac ccc	2064
Glu Met Leu Ala Arg Phe Val Val Gly Ser His Val Arg His His Pro	
675 680 685	
agt aac aag aag gat gaa ggg ttg act aat ggt ggc acc ttg gag cca	2112
Ser Asn Lys Lys Asp Glu Gly Leu Thr Asn Gly Gly Thr Leu Glu Pro	
690 695 700	
gcc atg ccc aac aca tat ggc gtg gag ccc ctg cct cag gag gtg ctg	2160
Ala Met Pro Asn Thr Tyr Gly Val Glu Pro Leu Pro Gln Glu Val Leu	
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Lys Lys Tyr Ile Ile Tyr Ala Lys Glu Arg Val Arg Pro Lys Leu Asn	
725 730 735	
cag atg gac cag gat aaa gtg gcc agg atg tac agt gac ctg agg aag	2256
Gln Met Asp Gln Asp Lys Val Ala Arg Met Tyr Ser Asp Leu Arg Lys	
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Glu Ser Met Ala Thr Gly Ser Ile Pro Ile Thr Val Arg His Ile Glu	
755 760 765	
tcc atg atc cgc atg gcc gag gcc cat gcc cgc atg cac ctg cgg gac	2352
Ser Met Ile Arg Met Ala Glu Ala His Ala Arg Met His Leu Arg Asp	
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Tyr Val Met Glu Asp Asp Val Asn Met Ala Ile Arg Val Met Met Glu	
785 790 795 800	
agc ttc att gac acc cag aag ttc agc gtc atg cgg agt atg cgc aag	2448
Ser Phe Ile Asp Thr Gln Lys Phe Ser Val Met Arg Ser Met Arg Lys	
805 810 815	
act ttt gcc cgg tat ctc tcc ttc cgg cga gat aac aat gat ctg ctg	2496
Thr Phe Ala Arg Tyr Leu Ser Phe Arg Arg Asp Asn Asn Asp Leu Leu	
820 825 830	
ctc ttc ata ctg aag cag ttg gtg gct gag cag gtg aca tat caa cgc	2544
Leu Phe Ile Leu Lys Gln Leu Val Ala Glu Gln Val Thr Tyr Gln Arg	
835 840 845	
aac cgc ttt ggg gcc cag cag gac acc att gaa ata cct gag aag gat	2592
Asn Arg Phe Gly Ala Gln Gln Asp Thr Ile Glu Ile Pro Glu Lys Asp	
850 855 860	
ctg atg gac aag gcc agg cag atc aat att cac aac ctc tct gcc ttc	2640
Leu Met Asp Lys Ala Arg Gln Ile Asn Ile His Asn Leu Ser Ala Phe	
865 870 875 880	

tac	gac	agc	gac	ctc	ttc	aaa	ttc	aac	aag	ttc	agc	cgt	gac	ctg	aaa	2688
Tyr	Asp	Ser	Asp	Leu	Phe	Lys	Phe	Asn	Lys	Phe	Ser	Arg	Asp	Leu	Lys	
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Arg Lys Leu Ile Leu Gln Gln Phe  
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<212> PRT
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Arg	Arg	Ala	Asp	Ala	Leu	Thr	Ser	Ser	Pro	Gly	Arg	Asp	Leu	Pro	Pro
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Phe	Glu	Asp	Glu	Ser	Glu	Gly	Leu	Leu	Gly	Thr	Glu	Gly	Pro	Met	Glu
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Tyr	Arg	Pro	Ile	Pro	Glu	Leu	Asp	Val	Tyr	Glu	Ala	Glu	Gly	Leu	Ala
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Leu	Asp	Asp	Glu	Asp	Val	Glu	Glu	Leu	Thr	Ala	Ser	Gln	Arg	Glu	Ala
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Ala	Glu	Arg	Thr	Met	Arg	Gln	Arg	Asp	Arg	Glu	Ala	Gly	Arg	Gly	Leu
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Glu	Arg	Pro	Ala	Arg	Lys	Arg	Arg	His	Val	Glu	Arg	Ala	Thr	Glu	Asp
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Gly	Glu	Glu	Asp	Glu	Glu	Met	Ile	Glu	Ser	Ile	Glu	Asn	Leu	Glu	Asp
				165					170					175	
Leu	Lys	Gly	His	Ser	Val	Arg	Glu	Arg	Val	Ser	Met	Ala	Gly	Pro	Arg
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Leu	Glu	Ile	His	His	Arg	Phe	Lys	Asn	Phe	Leu	Arg	Thr	His	Val	Asp
		195					200					205			
Ser	His	Gly	His	Asn	Val	Phe	Lys	Glu	Arg	Ile	Ser	Asp	Met	Cys	Lys
	210					215					220				
Glu	Asn	Arg	Glu	Ser	Leu	Val	Val	Asn	Tyr	Glu	Asp	Leu	Ala	Ala	Arg
225				230						235					240
Glu	His	Val	Leu	Ala	Tyr	Phe	Leu	Pro	Glu	Ala	Pro	Ala	Glu	Leu	Leu
				245					250					255	
Gln	Ile	Phe	Asp	Glu	Ala	Ala	Leu	Glu	Val	Val	Leu	Ala	Met	Tyr	Pro
			260					265					270		
Lys	Tyr	Asp	Arg	Ile	Thr	Asn	His	Ile	His	Val	Arg	Ile	Ser	His	Leu
		275					280					285			
Pro	Leu	Val	Glu	Glu	Leu	Arg	Ser	Leu	Arg	Gln	Leu	His	Leu	Asn	Gln
	290					295					300				
Leu	Ile	Arg	Thr	Ser	Gly	Val	Val	Thr	Ser	Cys	Thr	Gly	Val	Leu	Pro
305					310					315					320
Gln	Leu	Ser	Met	Val	Lys	Tyr	Asn	Cys	Ser	Lys	Cys	Asn	Phe	Val	Leu
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Gly	Pro	Phe	Cys	Gln	Ser	Gln	Asn	Gln	Glu	Val	Lys	Pro	Gly	Ser	Cys
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Ile	Tyr	Gln	Asn	Tyr	Gln	Arg	Ile	Arg	Ile	Gln	Glu	Ser	Pro	Gly	Lys	370	375	380
Val	Ala	Ala	Gly	Arg	Leu	Pro	Arg	Ser	Lys	Asp	Ala	Ile	Leu	Leu	Ala	385	390	395
Asp	Leu	Val	Asp	Ser	Cys	Lys	Pro	Gly	Asp	Glu	Ile	Glu	Leu	Thr	Gly	405	410	415
Ile	Tyr	His	Asn	Asn	Tyr	Asp	Gly	Ser	Leu	Asn	Thr	Ala	Asn	Gly	Phe	420	425	430
Pro	Val	Phe	Ala	Thr	Ile	Ile	Leu	Ala	Asn	His	Val	Ala	Lys	Lys	Asp	435	440	445
Asn	Lys	Val	Ala	Val	Gly	Glu	Leu	Thr	Asp	Glu	Asp	Val	Lys	Met	Ile	450	455	460
Thr	Gly	Leu	Ser	Lys	Asp	Gln	Gln	Ile	Gly	Glu	Lys	Ile	Phe	Ala	Ser	465	470	475
Ile	Ala	Pro	Ser	Ile	Tyr	Gly	His	Glu	Asp	Ile	Lys	Arg	Gly	Leu	Ala	485	490	495
Leu	Ala	Leu	Phe	Gly	Gly	Glu	Pro	Lys	Asn	Pro	Gly	Gly	Lys	His	Lys	500	505	510
Val	Arg	Gly	Asp	Ile	Asn	Val	Leu	Leu	Cys	Gly	Asp	Pro	Gly	Thr	Ala	515	520	525
Lys	Ser	Gln	Phe	Leu	Lys	Tyr	Ile	Glu	Lys	Val	Ser	Ser	Arg	Ala	Ile	530	535	540
Phe	Thr	Thr	Gly	Gln	Gly	Ala	Ser	Ala	Val	Gly	Leu	Thr	Ala	Tyr	Val	545	550	555
Gln	Arg	His	Pro	Val	Ser	Arg	Glu	Trp	Thr	Leu	Glu	Ala	Gly	Ala	Leu	565	570	575
Val	Leu	Ala	Asp	Arg	Gly	Val	Cys	Leu	Ile	Asp	Glu	Phe	Asp	Lys	Met	580	585	590
Asn	Asp	Gln	Asp	Arg	Thr	Ser	Ile	His	Glu	Ala	Met	Glu	Gln	Gln	Ser	595	600	605
Ile	Ser	Ile	Ser	Lys	Ala	Gly	Ile	Val	Thr	Ser	Leu	Gln	Ala	Arg	Cys	610	615	620
Thr	Val	Ile	Ala	Ala	Ala	Asn	Pro	Ile	Gly	Gly	Arg	Tyr	Asp	Pro	Ser	625	630	635
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Phe	Asp	Val	Leu	Cys	Val	Val	Arg	Asp	Thr	Val	Asp	Pro	Val	Gln	Asp	660	665	670
Glu	Met	Leu	Ala	Arg	Phe	Val	Val	Gly	Ser	His	Val	Arg	His	His	Pro	675	680	685
Ser	Asn	Lys	Lys	Asp	Glu	Gly	Leu	Thr	Asn	Gly	Gly	Thr	Leu	Glu	Pro	690	695	700
Ala	Met	Pro	Asn	Thr	Tyr	Gly	Val	Glu	Pro	Leu	Pro	Gln	Glu	Val	Leu	705	710	715
Lys	Lys	Tyr	Ile	Ile	Tyr	Ala	Lys	Glu	Arg	Val	Arg	Pro	Lys	Leu	Asn	725	730	735
Gln	Met	Asp	Gln	Asp	Lys	Val	Ala	Arg	Met	Tyr	Ser	Asp	Leu	Arg	Lys	740	745	750
Glu	Ser	Met	Ala	Thr	Gly	Ser	Ile	Pro	Ile	Thr	Val	Arg	His	Ile	Glu	755	760	765
Ser	Met	Ile	Arg	Met	Ala	Glu	Ala	His	Ala	Arg	Met	His	Leu	Arg	Asp	770	775	780
Tyr	Val	Met	Glu	Asp	Asp	Val	Asn	Met	Ala	Ile	Arg	Val	Met	Met	Glu	785	790	795
Ser	Phe	Ile	Asp	Thr	Gln	Lys	Phe	Ser	Val	Met	Arg	Ser	Met	Arg	Lys	805	810	815
Thr	Phe	Ala	Arg	Tyr	Leu	Ser	Phe	Arg	Arg	Asp	Asn	Asn	Asp	Leu	Leu	820	825	830
Leu	Phe	Ile	Leu	Lys	Gln	Leu	Val	Ala	Glu	Gln	Val	Thr	Tyr	Gln	Arg	835	840	845

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Asn Arg Phe Gly Ala Gln Gln Asp Thr Ile Glu Ile Pro Glu Lys Asp
 850                               855                               860
Leu Met Asp Lys Ala Arg Gln Ile Asn Ile His Asn Leu Ser Ala Phe
865                               870                               875                               880
Tyr Asp Ser Asp Leu Phe Lys Phe Asn Lys Phe Ser Arg Asp Leu Lys
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aattggcttg tg atg gag gcg tct ttg ggg att cag atg gat gag cca atg 171
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gct ttt tct ccc cag cgt gac cgg ttt cag gct gaa ggc tct tta aaa 219
Ala Phe Ser Pro Gln Arg Asp Arg Phe Gln Ala Glu Gly Ser Leu Lys
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aaa aac gag cag aat ttt aaa ctt gca ggt gtt aaa aaa gat att gag 267
Lys Asn Glu Gln Asn Phe Lys Leu Ala Gly Val Lys Lys Asp Ile Glu
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aag ctt tat gaa gct gta cca cag ctt agt aat gtg ttt aag att gag 315
Lys Leu Tyr Glu Ala Val Pro Gln Leu Ser Asn Val Phe Lys Ile Glu
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gac aaa att gga gaa ggc act ttc agc tct gtt tat ttg gcc aca gca 363
Asp Lys Ile Gly Glu Gly Thr Phe Ser Ser Val Tyr Leu Ala Thr Ala
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cag tta caa gta gga cct gaa gag aaa att gct cta aaa cac ttg att 411
Gln Leu Gln Val Gly Pro Glu Glu Lys Ile Ala Leu Lys His Leu Ile
          80              85              90

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cca aca agt cat cct ata aga att gca gct gaa ctt cag tgc cta aca 459
Pro Thr Ser His Pro Ile Arg Ile Ala Ala Glu Leu Gln Cys Leu Thr
          95              100              105

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gtg gct ggg ggg caa gat aat gtc atg gga gtt aaa tac tgc ttt agg 507
Val Ala Gly Gly Gln Asp Asn Val Met Gly Val Lys Tyr Cys Phe Arg
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aag aat gat cat gta gtt att gct atg cca tat ctg gag cat gag tcg 555
Lys Asn Asp His Val Val Ile Ala Met Pro Tyr Leu Glu His Glu Ser
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Phe Leu Asp Ile Leu Asn Ser Leu Ser Phe Gln Glu Val Arg Glu Tyr	
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Met Leu Asn Leu Phe Lys Ala Leu Lys Arg Ile His Gln Phe Gly Ile	
160 165 170	
gtt cac cgt gat gtt aag ccc agc aat ttt tta tat aat agg cgc ctg	699
Val His Arg Asp Val Lys Pro Ser Asn Phe Leu Tyr Asn Arg Arg Leu	
175 180 185	
aaa aag tat gcc ttg gta gac ttt ggt ttg gcc caa gga acc cat gat	747
Lys Lys Tyr Ala Leu Val Asp Phe Gly Leu Ala Gln Gly Thr His Asp	
190 195 200 205	
acg aaa ata gag ctt ctt aaa ttt gtc cag tct gaa gct cag cag gaa	795
Thr Lys Ile Glu Leu Leu Lys Phe Val Gln Ser Glu Ala Gln Gln Glu	
210 215 220	
agg tgt tca caa aac aaa tcc cac ata atc aca gga aac aag att cca	843
Arg Cys Ser Gln Asn Lys Ser His Ile Ile Thr Gly Asn Lys Ile Pro	
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Leu Ser Gly Pro Val Pro Lys Glu Leu Asp Gln Gln Ser Thr Thr Lys	
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Ala Ser Val Lys Arg Pro Tyr Thr Asn Ala Gln Ile Gln Ile Lys Gln	
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gga aaa gac gga aag gag gga tct gta ggc ctt tct gtc cag cgc tct	987
Gly Lys Asp Gly Lys Glu Gly Ser Val Gly Leu Ser Val Gln Arg Ser	
270 275 280 285	
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Val Phe Gly Glu Arg Asn Phe Asn Ile His Ser Ser Ile Ser His Glu	
290 295 300	
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Ser Pro Ala Val Lys Leu Met Lys Gln Ser Lys Thr Val Asp Val Leu	
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Ser Arg Lys Leu Ala Thr Lys Lys Lys Ala Ile Ser Thr Lys Val Met	
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Asn Ser Ala Val Met Arg Lys Thr Ala Ser Ser Cys Pro Ala Ser Leu	
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acc tgt gac tgc tat gca aca gat aaa gtt tgt agt att tgc ctt tca	1227
Thr Cys Asp Cys Tyr Ala Thr Asp Lys Val Cys Ser Ile Cys Leu Ser	
350 355 360 365	
agg cgt cag cag gtt gcc cct agg gca ggt aca cca gga ttc aga gca	1275
Arg Arg Gln Gln Val Ala Pro Arg Ala Gly Thr Pro Gly Phe Arg Ala	
370 375 380	

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Pro Glu Val Leu Thr Lys Cys Pro Asn Gln Thr Thr Ala Ile Asp Met	
385 390 395	
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Phe Tyr Lys Ala Ser Asp Asp Leu Thr Ala Leu Ala Gln Ile Met Thr	
415 420 425	
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Ile Arg Gly Ser Arg Glu Thr Ile Gln Ala Ala Lys Thr Phe Gly Lys	
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Ser Ile Leu Cys Ser Lys Glu Val Pro Ala Gln Asp Leu Arg Lys Leu	
450 455 460	
tgt gag aga ctc agg ggt atg gat tct agc act ccc aag tta aca agt	1563
Cys Glu Arg Leu Arg Gly Met Asp Ser Ser Thr Pro Lys Leu Thr Ser	
465 470 475	
gat ata caa ggg cat gct tct cat caa cca gct att tca gag aag act	1611
Asp Ile Gln Gly His Ala Ser His Gln Pro Ala Ile Ser Glu Lys Thr	
480 485 490	
gac cat aaa gct tct tgc ctc gtt caa aca cct cca gga caa tac tca	1659
Asp His Lys Ala Ser Cys Leu Val Gln Thr Pro Pro Gly Gln Tyr Ser	
495 500 505	
ggg aat tca ttt aaa aag ggg gat agt aat agc tgt gag cat tgt ttt	1707
Gly Asn Ser Phe Lys Lys Gly Asp Ser Asn Ser Cys Glu His Cys Phe	
510 515 520 525	
gat gag tat aat acc aat tta gaa ggc tgg aat gag gta cct gat gaa	1755
Asp Glu Tyr Asn Thr Asn Leu Glu Gly Trp Asn Glu Val Pro Asp Glu	
530 535 540	
gct tat gac ctg ctt gat aaa ctt cta gat cta aat cca gct tca aga	1803
Ala Tyr Asp Leu Leu Asp Lys Leu Leu Asp Leu Asn Pro Ala Ser Arg	
545 550 555	
ata aca gca gaa gaa gct ttg ttg cat cca ttt ttt aaa gat atg agc	1851
Ile Thr Ala Glu Glu Ala Leu Leu His Pro Phe Phe Lys Asp Met Ser	
560 565 570	
ttg tga taatggatct tcatttaatg tttactgtta tgaggtagaa taaaaaagaa	1907
Leu	
tactttgttaa tagccacaag ttcttggtta gagaccagag caggattaat aatttatattt	1967
aacatttttag tgtttggtgg cacatttctaa aatatagatt aagaatactt aaaatgcctg	2027
ggatagttct tgggactaac aacatgatct tctttgagtt aaacctacct aagtagattt	2087
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gaaactcaac ctggtgctgg tgctcttaac aattttgttaa ataaagaaga taatttcctt	2327
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ggggcaagt atcacttaaa attgaattca tccattttta aaaaacactt catgaaagca	2447
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gttatccttt tatatttttt 3187

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&lt;210&gt; 7

&lt;211&gt; 574

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 7

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Met Glu Ala Ser Leu Gly Ile Gln Met Asp Glu Pro Met Ala Phe Ser
1          5          10          15
Pro Gln Arg Asp Arg Phe Gln Ala Glu Gly Ser Leu Lys Lys Asn Glu
20          25          30
Gln Asn Phe Lys Leu Ala Gly Val Lys Lys Asp Ile Glu Lys Leu Tyr
35          40          45
Glu Ala Val Pro Gln Leu Ser Asn Val Phe Lys Ile Glu Asp Lys Ile
50          55          60
Gly Glu Gly Thr Phe Ser Ser Val Tyr Leu Ala Thr Ala Gln Leu Gln
65          70          75          80
Val Gly Pro Glu Glu Lys Ile Ala Leu Lys His Leu Ile Pro Thr Ser
85          90          95
His Pro Ile Arg Ile Ala Ala Glu Leu Gln Cys Leu Thr Val Ala Gly
100          105          110
Gly Gln Asp Asn Val Met Gly Val Lys Tyr Cys Phe Arg Lys Asn Asp
115          120          125
His Val Val Ile Ala Met Pro Tyr Leu Glu His Glu Ser Phe Leu Asp
130          135          140
Ile Leu Asn Ser Leu Ser Phe Gln Glu Val Arg Glu Tyr Met Leu Asn
145          150          155          160
Leu Phe Lys Ala Leu Lys Arg Ile His Gln Phe Gly Ile Val His Arg
165          170          175
Asp Val Lys Pro Ser Asn Phe Leu Tyr Asn Arg Arg Leu Lys Lys Tyr
180          185          190
Ala Leu Val Asp Phe Gly Leu Ala Gln Gly Thr His Asp Thr Lys Ile
195          200          205
Glu Leu Leu Lys Phe Val Gln Ser Glu Ala Gln Gln Glu Arg Cys Ser
210          215          220
Gln Asn Lys Ser His Ile Ile Thr Gly Asn Lys Ile Pro Leu Ser Gly
225          230          235          240
Pro Val Pro Lys Glu Leu Asp Gln Gln Ser Thr Thr Lys Ala Ser Val
245          250          255
Lys Arg Pro Tyr Thr Asn Ala Gln Ile Gln Ile Lys Gln Gly Lys Asp
260          265          270
Gly Lys Glu Gly Ser Val Gly Leu Ser Val Gln Arg Ser Val Phe Gly
275          280          285
Glu Arg Asn Phe Asn Ile His Ser Ser Ile Ser His Glu Ser Pro Ala
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Val Lys Leu Met Lys Gln Ser Lys Thr Val Asp Val Leu Ser Arg Lys
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ggccagagcg	aggcgcgaga	aggacggcgg	cgtgaggggg	cggggcgcg	agcgcgagaa	180										
ggcaggcacg	aggggcgagc	gcgaggcggg	gcacggcgcg	tggcgtgaga	cggggcgggg	240										
cgcgcgatc	ggcgccgcgg	ccgcgtgacg	cgttttcaa	tcttcaaccg	ccgcagccca	300										
ctcgtttgtg	ctttgcgcct	tctctctcgc	cgccttggag	ccggaatccg	ccccggaaac	360										
ccgacctgca	gacgcggtac	ctctactgcg	tagaggccgt	agctggcgga	aggagagagg	420										
cggccgtcct	gtcaacaggc	cgggggaagc	cgtgctttcg	cggctgccc	gtgcgacact	480										
ttctccggac					ccagcatgta	ggtgccgggc	gactgcc	atg	aac	tcc	gga	gcc	atg	535		
								Met	Asn	Ser	Gly	Ala	Met			
								1							5	
agg	atc	cac	agt	aaa	gga	cat	ttc	cag	ggt	gga	atc	caa	gtc	aaa	aat	583
Arg	Ile	His	Ser	Lys	Gly	His	Phe	Gln	Gly	Gly	Ile	Gln	Val	Lys	Asn	
				10					15					20		

gaa	aaa	aac	aga	cca	tct	ctg	aaa	tct	ctg	aaa	act	gat	aac	agg	cca	631
Glu	Lys	Asn	Arg	Pro	Ser	Leu	Lys	Ser	Leu	Lys	Thr	Asp	Asn	Arg	Pro	
		25					30					35				
gaa	aaa	tcc	aaa	tgt	aag	cca	ctt	tgg	gga	aaa	gta	ttt	tac	ctt	gac	679
Glu	Lys	Ser	Lys	Cys	Lys	Pro	Leu	Trp	Gly	Lys	Val	Phe	Tyr	Leu	Asp	
	40					45					50					
tta	cct	tct	gtc	acc	ata	tct	gaa	aaa	ctt	caa	aag	gac	att	aag	gat	727
Leu	Pro	Ser	Val	Thr	Ile	Ser	Glu	Lys	Leu	Gln	Lys	Asp	Ile	Lys	Asp	
	55				60					65					70	
ctg	gga	ggg	cga	gtt	gaa	gaa	ttt	ctc	agc	aaa	gat	atc	agt	tat	ctt	775
Leu	Gly	Gly	Arg	Val	Glu	Glu	Phe	Leu	Ser	Lys	Asp	Ile	Ser	Tyr	Leu	
			75					80						85		
att	tca	aat	aag	aag	gaa	gct	aaa	ttt	gca	caa	acc	ttg	ggt	cga	att	823
Ile	Ser	Asn	Lys	Lys	Glu	Ala	Lys	Phe	Ala	Gln	Thr	Leu	Gly	Arg	Ile	
		90					95						100			
tct	cct	gta	cca	agt	cca	gaa	tct	gca	tat	act	gca	gaa	acc	act	tca	871
Ser	Pro	Val	Pro	Ser	Pro	Glu	Ser	Ala	Tyr	Thr	Ala	Glu	Thr	Thr	Ser	
	105					110						115				
cct	cat	ccc	agc	cat	gat	gga	agt	tca	ttt	aag	tca	cca	gac	aca	gtg	919
Pro	His	Pro	Ser	His	Asp	Gly	Ser	Ser	Phe	Lys	Ser	Pro	Asp	Thr	Val	
	120					125					130					
tgt	tta	agc	aga	gga	aaa	tta	tta	gtt	gaa	aaa	gct	atc	aag	gac	cat	967
Cys	Leu	Ser	Arg	Gly	Lys	Leu	Leu	Val	Glu	Lys	Ala	Ile	Lys	Asp	His	
	135				140					145				150		
gat	ttt	att	cct	tca	aat	agt	ata	tta	tca	aat	gcc	ttg	tca	tgg	gga	1015
Asp	Phe	Ile	Pro	Ser	Asn	Ser	Ile	Leu	Ser	Asn	Ala	Leu	Ser	Trp	Gly	
				155				160						165		
gta	aaa	att	ctt	cat	att	gat	gac	att	aga	tac	tac	att	gaa	caa	aag	1063
Val	Lys	Ile	Leu	His	Ile	Asp	Asp	Ile	Arg	Tyr	Tyr	Ile	Glu	Gln	Lys	
		170					175						180			
aaa	aaa	gag	ttg	tat	tta	ctc	aag	aaa	tca	agt	act	tca	gta	aga	gat	1111
Lys	Lys	Glu	Leu	Tyr	Leu	Leu	Lys	Lys	Ser	Ser	Thr	Ser	Val	Arg	Asp	
		185					190					195				
ggg	ggc	aaa	aga	gtt	ggt	agt	ggt	gca	caa	aaa	aca	aga	aca	gga	aga	1159
Gly	Gly	Lys	Arg	Val	Gly	Ser	Gly	Ala	Gln	Lys	Thr	Arg	Thr	Gly	Arg	
	200					205					210					
ctc	aaa	aag	cct	ttt	gta	aag	gtg	gaa	gat	atg	agc	caa	ctt	tat	agg	1207
Leu	Lys	Lys	Pro	Phe	Val	Lys	Val	Glu	Asp	Met	Ser	Gln	Leu	Tyr	Arg	
	215				220					225					230	
cca	ttt	tat	ctt	cag	ctg	acc	aat	atg	cct	ttt	ata	aat	tat	tct	att	1255
Pro	Phe	Tyr	Leu	Gln	Leu	Thr	Asn	Met	Pro	Phe	Ile	Asn	Tyr	Ser	Ile	
				235				240						245		
cag	aag	ccc	tgc	agt	cca	ttt	gat	gta	gac	aag	cca	tct	agt	atg	caa	1303
Gln	Lys	Pro	Cys	Ser	Pro	Phe	Asp	Val	Asp	Lys	Pro	Ser	Ser	Met	Gln	
		250						255					260			

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Lys	Gln	Thr	Gln	Val	Lys	Leu	Arg	Ile	Gln	Thr	Asp	Gly	Asp	Lys	Tyr	
		265					270					275				
ggt	gga	acc	tca	att	caa	ctc	cag	ttg	aaa	gag	aag	aag	aaa	aaa	gga	1399
Gly	Gly	Thr	Ser	Ile	Gln	Leu	Gln	Leu	Lys	Glu	Lys	Lys	Lys	Lys	Gly	
	280					285					290					
tat	tgt	gaa	tgt	tgc	ttg	cag	aaa	tat	gaa	gat	cta	gaa	act	cac	ctt	1447
Tyr	Cys	Glu	Cys	Cys	Leu	Gln	Lys	Tyr	Glu	Asp	Leu	Glu	Thr	His	Leu	
295					300					305					310	
cta	agt	gag	caa	cac	aga	aac	ttt	gca	cag	agt	aac	cag	tat	caa	gtt	1495
Leu	Ser	Glu	Gln	His	Arg	Asn	Phe	Ala	Gln	Ser	Asn	Gln	Tyr	Gln	Val	
				315					320					325		
gtt	gat	gat	att	gta	tct	aag	tta	gtt	ttt	gac	ttt	gtg	gaa	tat	gaa	1543
Val	Asp	Asp	Ile	Val	Ser	Lys	Leu	Val	Phe	Asp	Phe	Val	Glu	Tyr	Glu	
			330					335					340			
aag	gac	aca	cct	aaa	aag	aaa	aga	ata	aaa	tac	agt	gtt	gga	tcc	ctt	1591
Lys	Asp	Thr	Pro	Lys	Lys	Lys	Arg	Ile	Lys	Tyr	Ser	Val	Gly	Ser	Leu	
		345					350					355				
tct	cct	gtt	tct	gca	agt	gtc	ctg	aaa	aag	act	gaa	caa	aag	gaa	aaa	1639
Ser	Pro	Val	Ser	Ala	Ser	Val	Leu	Lys	Lys	Thr	Glu	Gln	Lys	Glu	Lys	
	360					365					370					
gtg	gaa	ttg	caa	cat	att	tct	cag	aaa	gat	tgc	cag	gaa	gat	gat	aca	1687
Val	Glu	Leu	Gln	His	Ile	Ser	Gln	Lys	Asp	Cys	Gln	Glu	Asp	Asp	Thr	
375					380					385					390	
aca	gtg	aag	gag	cag	aat	ttc	ctg	tat	aaa	gag	acc	cag	gaa	act	gaa	1735
Thr	Val	Lys	Glu	Gln	Asn	Phe	Leu	Tyr	Lys	Glu	Thr	Gln	Glu	Thr	Glu	
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Lys	Lys	Leu	Leu	Phe	Ile	Ser	Glu	Pro	Ile	Pro	His	Pro	Ser	Asn	Glu	
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Leu	Arg	Gly	Leu	Asn	Glu	Lys	Met	Ser	Asn	Lys	Cys	Ser	Met	Leu	Ser	
		425					430					435				
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Thr	Ala	Glu	Asp	Asp	Ile	Arg	Gln	Asn	Phe	Thr	Gln	Leu	Pro	Leu	His	
	440					445					450					
aaa	aac	aaa	cag	gaa	tgc	att	ctt	gac	att	tcc	gaa	cac	aca	tta	agt	1927
Lys	Asn	Lys	Gln	Glu	Cys	Ile	Leu	Asp	Ile	Ser	Glu	His	Thr	Leu	Ser	
455					460					465					470	
gaa	aat	gac	tta	gaa	gaa	cta	agg	gta	gat	cac	tat	aaa	tgt	aac	ata	1975
Glu	Asn	Asp	Leu	Glu	Glu	Leu	Arg	Val	Asp	His	Tyr	Lys	Cys	Asn	Ile	
			475					480						485		
cag	gca	tct	gta	cat	gtt	tct	gat	ttc	agt	aca	gat	aat	agt	gga	tct	2023
Gln	Ala	Ser	Val	His	Val	Ser	Asp	Phe	Ser	Thr	Asp	Asn	Ser	Gly	Ser	
			490					495						500		

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Gln Pro Lys Gln Lys Ser Asp Thr Val Leu Phe Pro Ala Lys Asp Leu
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aag gaa aag gac ctt cat tca ata ttt act cat gat tct ggt ctg ata 2119
Lys Glu Lys Asp Leu His Ser Ile Phe Thr His Asp Ser Gly Leu Ile
      520                      525                      530

aca ata aac agt tca caa gag cac cta act gtt cag gca aag gct cca 2167
Thr Ile Asn Ser Ser Gln Glu His Leu Thr Val Gln Ala Lys Ala Pro
      535                      540                      545                      550

ttc cat act cct cct gag gaa ccc aat gaa tgt gac ttc aag aat atg 2215
Phe His Thr Pro Pro Glu Glu Pro Asn Glu Cys Asp Phe Lys Asn Met
      555                      560                      565

gat agt tta cct tct ggt aaa ata cat cga aaa gtg aaa ata ata tta 2263
Asp Ser Leu Pro Ser Gly Lys Ile His Arg Lys Val Lys Ile Ile Leu
      570                      575                      580

gga cga aat aga aaa gaa aat ctg gaa cca aat gct gaa ttt gat aaa 2311
Gly Arg Asn Arg Lys Glu Asn Leu Glu Pro Asn Ala Glu Phe Asp Lys
      585                      590                      595

aga act gaa ttt att aca caa gaa gaa aac aga att tgt agt tca ccg 2359
Arg Thr Glu Phe Ile Thr Gln Glu Glu Asn Arg Ile Cys Ser Ser Pro
      600                      605                      610

gta cag tct tta cta gac ttg ttt cag act agt gaa gag aaa tca gaa 2407
Val Gln Ser Leu Leu Asp Leu Phe Gln Thr Ser Glu Glu Lys Ser Glu
      615                      620                      625                      630

ttt ttg ggt ttc aca agc tac aca gaa aag agt ggt ata tgc aat gtt 2455
Phe Leu Gly Phe Thr Ser Tyr Thr Glu Lys Ser Gly Ile Cys Asn Val
      635                      640                      645

tta gat att tgg gaa gag gaa aat tca gat aat ctg tta aca gcg ttt 2503
Leu Asp Ile Trp Glu Glu Glu Asn Ser Asp Asn Leu Leu Thr Ala Phe
      650                      655                      660

ttc tcg tcc cct tca act tct aca ttt act ggc ttt tag aatttaaaaa 2552
Phe Ser Ser Pro Ser Thr Ser Thr Phe Thr Gly Phe
      665                      670

atgcatactt ttcagaagtg ataaggatca tattcttgaa attttttataa atatgtatgg 2612
aaattcttag gatttttttta ccagctttgt ttacagaccc aaatgtaaat attaaaaata 2672
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&lt;210&gt; 9

&lt;211&gt; 674

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 9

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Met Asn Ser Gly Ala Met Arg Ile His Ser Lys Gly His Phe Gln Gly
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Gly Ile Gln Val Lys Asn Glu Lys Asn Arg Pro Ser Leu Lys Ser Leu
      20          25          30

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Lys	Asp	Ile	Ser	Tyr	Leu	Ile	Ser	Asn	Lys	Lys	Glu	Ala	Lys	Phe	Ala	85	90	95
Gln	Thr	Leu	Gly	Arg	Ile	Ser	Pro	Val	Pro	Ser	Pro	Glu	Ser	Ala	Tyr	100	105	110
Thr	Ala	Glu	Thr	Thr	Ser	Pro	His	Pro	Ser	His	Asp	Gly	Ser	Ser	Phe	115	120	125
Lys	Ser	Pro	Asp	Thr	Val	Cys	Leu	Ser	Arg	Gly	Lys	Leu	Leu	Val	Glu	130	135	140
Lys	Ala	Ile	Lys	Asp	His	Asp	Phe	Ile	Pro	Ser	Asn	Ser	Ile	Leu	Ser	145	150	155
Asn	Ala	Leu	Ser	Trp	Gly	Val	Lys	Ile	Leu	His	Ile	Asp	Asp	Ile	Arg	165	170	175
Tyr	Tyr	Ile	Glu	Gln	Lys	Lys	Lys	Glu	Leu	Tyr	Leu	Leu	Lys	Lys	Ser	180	185	190
Ser	Thr	Ser	Val	Arg	Asp	Gly	Gly	Lys	Arg	Val	Gly	Ser	Gly	Ala	Gln	195	200	205
Lys	Thr	Arg	Thr	Gly	Arg	Leu	Lys	Lys	Pro	Phe	Val	Lys	Val	Glu	Asp	210	215	220
Met	Ser	Gln	Leu	Tyr	Arg	Pro	Phe	Tyr	Leu	Gln	Leu	Thr	Asn	Met	Pro	225	230	235
Phe	Ile	Asn	Tyr	Ser	Ile	Gln	Lys	Pro	Cys	Ser	Pro	Phe	Asp	Val	Asp	245	250	255
Lys	Pro	Ser	Ser	Met	Gln	Lys	Gln	Thr	Gln	Val	Lys	Leu	Arg	Ile	Gln	260	265	270
Thr	Asp	Gly	Asp	Lys	Tyr	Gly	Gly	Thr	Ser	Ile	Gln	Leu	Gln	Leu	Lys	275	280	285
Glu	Lys	Lys	Lys	Lys	Gly	Tyr	Cys	Glu	Cys	Cys	Leu	Gln	Lys	Tyr	Glu	290	295	300
Asp	Leu	Glu	Thr	His	Leu	Leu	Ser	Glu	Gln	His	Arg	Asn	Phe	Ala	Gln	305	310	315
Ser	Asn	Gln	Tyr	Gln	Val	Val	Asp	Asp	Ile	Val	Ser	Lys	Leu	Val	Phe	325	330	335
Asp	Phe	Val	Glu	Tyr	Glu	Lys	Asp	Thr	Pro	Lys	Lys	Lys	Arg	Ile	Lys	340	345	350
Tyr	Ser	Val	Gly	Ser	Leu	Ser	Pro	Val	Ser	Ala	Ser	Val	Leu	Lys	Lys	355	360	365
Thr	Glu	Gln	Lys	Glu	Lys	Val	Glu	Leu	Gln	His	Ile	Ser	Gln	Lys	Asp	370	375	380
Cys	Gln	Glu	Asp	Asp	Thr	Thr	Val	Lys	Glu	Gln	Asn	Phe	Leu	Tyr	Lys	385	390	395
Glu	Thr	Gln	Glu	Thr	Glu	Lys	Lys	Leu	Leu	Phe	Ile	Ser	Glu	Pro	Ile	405	410	415
Pro	His	Pro	Ser	Asn	Glu	Leu	Arg	Gly	Leu	Asn	Glu	Lys	Met	Ser	Asn	420	425	430
Lys	Cys	Ser	Met	Leu	Ser	Thr	Ala	Glu	Asp	Asp	Ile	Arg	Gln	Asn	Phe	435	440	445
Thr	Gln	Leu	Pro	Leu	His	Lys	Asn	Lys	Gln	Glu	Cys	Ile	Leu	Asp	Ile	450	455	460
Ser	Glu	His	Thr	Leu	Ser	Glu	Asn	Asp	Leu	Glu	Glu	Leu	Arg	Val	Asp	465	470	475
His	Tyr	Lys	Cys	Asn	Ile	Gln	Ala	Ser	Val	His	Val	Ser	Asp	Phe	Ser	485	490	495
Thr	Asp	Asn	Ser	Gly	Ser	Gln	Pro	Lys	Gln	Lys	Ser	Asp	Thr	Val	Leu	500	505	510

Phe Pro Ala Lys Asp Leu Lys Glu Lys Asp Leu His Ser Ile Phe Thr  
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 His Asp Ser Gly Leu Ile Thr Ile Asn Ser Ser Gln Glu His Leu Thr  
           530                                  535                                  540  
 Val Gln Ala Lys Ala Pro Phe His Thr Pro Pro Glu Glu Pro Asn Glu  
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 Cys Asp Phe Lys Asn Met Asp Ser Leu Pro Ser Gly Lys Ile His Arg  
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 Lys Val Lys Ile Ile Leu Gly Arg Asn Arg Lys Glu Asn Leu Glu Pro  
                                   580                                  585                                  590  
 Asn Ala Glu Phe Asp Lys Arg Thr Glu Phe Ile Thr Gln Glu Glu Asn  
           595                                  600                                  605  
 Arg Ile Cys Ser Ser Pro Val Gln Ser Leu Leu Asp Leu Phe Gln Thr  
           610                                  615                                  620  
 Ser Glu Glu Lys Ser Glu Phe Leu Gly Phe Thr Ser Tyr Thr Glu Lys  
 625                                  630                                  635                                  640  
 Ser Gly Ile Cys Asn Val Leu Asp Ile Trp Glu Glu Glu Asn Ser Asp  
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 Asn Leu Leu Thr Ala Phe Phe Ser Ser Pro Ser Thr Ser Thr Phe Thr  
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 Gly Phe

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 <213> Homo sapiens

<400> 10  
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 Lys Lys Ser Ser Thr Ser Val Arg Asp Gly Gly Lys Arg Val Gly Ser  
                                   20                                  25                                  30  
 Gly Ala Gln Lys Thr Arg Thr Gly Arg Leu Lys Lys Pro Phe Val Lys  
                                   35                                  40                                  45  
 Val Glu Asp Met Ser Gln Leu Tyr Arg Pro Phe Tyr Leu Gln Leu Thr  
           50                                  55                                  60  
 Asn Met Pro Phe Ile Asn Tyr Ser Ile Gln Lys Pro Cys Ser Pro Phe  
   65                                  70                                  75                                  80  
 Asp Val Asp Lys Pro Ser Ser Met Gln Lys Gln Thr Gln Val Lys Leu  
                                   85                                  90                                  95  
 Arg Ile Gln Thr Asp Gly Asp Lys Tyr Gly Gly Thr Ser Ile Gln Leu  
                                   100                                  105                                  110  
 Gln Leu Lys Glu Lys Lys Lys Lys Gly Tyr Cys Glu Cys Cys Leu Gln  
           115                                  120                                  125  
 Lys Tyr Glu Asp Leu Glu Thr His Leu Leu Ser Glu Gln His Arg Asn  
           130                                  135                                  140  
 Phe Ala Gln Ser Asn Gln Tyr Gln Val Val Asp Asp Ile Val Ser Lys  
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 Leu Val Phe Asp Phe Val Glu Tyr Glu Lys Asp Thr Pro Lys Lys Lys  
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<210> 11  
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 <400> 12  
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 <210> 13  
 <211> 11  
 <212> PRT  
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 <400> 13  
 Tyr Gly Arg Lys Lys Arg Arg Gln Arg Arg Arg  
 1 5 10  
  
 <210> 14  
 <211> 12  
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<400> 15  
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<210> 16  
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<400> 16  
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<210> 17  
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<220>  
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<400> 17  
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<212> DNA  
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